

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Lee, Se-Jin
Huynh, Thanh
- (ii) TITLE OF THE INVENTION: GROWTH DIFFERENTIATION FACTOR-5
- (iii) NUMBER OF SEQUENCES: 27
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: Fish & Richardson, P.C.
 - (B) STREET: 4225 Executive Square, Suite 1400
 - (C) CITY: La Jolla
 - (D) STATE: CA
 - (E) COUNTRY: USA
 - (F) ZIP: 92037
-
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: Windows95
 - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER: 08/455,559
 - (B) FILING DATE: 31-MAY-1995
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER: 08/003,144
 - (B) FILING DATE: 12-JAN-1993
- (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: Lisa A. Haile, Ph.D.
 - (B) REGISTRATION NUMBER: 38,347
 - (C) REFERENCE/DOCKET NUMBER: 07265/057001
- (ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: 619/678-5070
 - (B) TELEFAX: 619/678-5099

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(vii) IMMEDIATE SOURCE:

(B) CLONE: 136

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCGGAATTCG GNTGGGARMG NTGGRTNR

28

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(vii) IMMEDIATE SOURCE:

(B) CLONE: 121

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1..42

(C) OTHER INFORMATION: / N at residue 13, 25 and 28 = Inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CCGGAATTCT CANCCRCAYT CRTCNACNAC CATRTCYTCT TA

42

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

(B) CLONE: 136

(ix) FEATURE:

(B) LOCATION: 1..7

(C) OTHER INFORMATION: Xaa at residue 4 = Arg or Ser; Xaa at residue 6 and 7 = Val, Ile or Met

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Gly Trp Glu Xaa Trp Xaa Xaa

1

5

- (A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(B) CLONE: 121

- Tyr Glu Asp Met Val Val Asp Glu Cys Gly Cys
1 5 10

[illegible]

- (A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(B) CLONE: 141

- (A) NAME/KEY: Coding Sequence
(B) LOCATION: 1..35
(C) OTHER INFORMATION: N at residue 12, 27, 30 and 33 = Inosine

- CCGGAATTCG GNTGGVANRA YTGGRTNRTN KCNCC

35

(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(B) CLONE: 145

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1..33
- (C) OTHER INFORMATION: N at residue 13, 19, 25 and 28 = Inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CCGGAATTCTCANSRCRANGMNTCNACNRYCAT

33

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

- (B) CLONE: 141

(ix) FEATURE:

- (B) LOCATION: 1..9
- (C) OTHER INFORMATION: Xaa at residue 3 = His, Gln, Asn, Lys, Glu or Asp; Xaa at residue 4 = Asp or Asn; Xaa at residues 6 and 7 = Val, Ile or Met; Xaa at residue 8 = Glu or Ser

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Gly Trp Xaa Xaa Trp Xaa Xaa Xaa Pro
 1 5

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

- (B) CLONE: 145

(ix) FEATURE:

- (B) LOCATION: 1..8
- (C) OTHER INFORMATION: Xaa at residues 2 and 3 = Val, Ile, Met, Thr or Ala; Xaa at residue 4 = Asp or Glu; Xaa at residue 5 = Ala or Ser; Xaa at residue 7 = Gly, Ala, Arg, Asn, Asp, Cys, Glu, Gln, His, Ile, Leu, Lys, Met, Phe Pro, Ser, Thr, Trp, Tyr, and Val.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Xaa Xaa Xaa Xaa Cys Xaa Cys
 1 5

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2329 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(vii) IMMEDIATE SOURCE:

- (B) CLONE: GD-5

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 322...1806

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TTCAAGCCCT CAGTCAGTTG TGCGGGAGAA AGGGGGCGGT CGGCTTTCTC CTTTCAAGAA	60
CGAGTTATTT TCAGCTGCTG ACTGGAGACG GTGCACGTCT GGACACGGGA GCACTTCCAC	120
TATGGGACTG GATACAGACA CACGCCCGGC GGAATTCAAG ACACTCAGAC TGAGGAGAAA	180
GCCCTGCCTG CTGCTGCTGC TGCTGCTGCT GCCACCGCTG CCTCTGAAGA CCCACTCCTT	240
TCATGGTTTT TCCTGCCAAG CCAGAGGCAC CTTGCTGCT ACGGCCTTTC TCTGTGGTGT	300
CATTCAGCGG CTGGCCAGAG G ATG AGA CTC CCC AAA CTC CTC ACT CTT TTG	351
Met Arg Leu Pro Lys Leu Leu Thr Leu Leu	
1 5 10	
CTG TGG CAC CTG GCT TGG CTG GAC CTG GAA CTC ATC TGC ACT GTG CTG	399
Leu Trp His Leu Ala Trp Leu Asp Leu Glu Leu Ile Cys Thr Val Leu	
15 20 25	
GGT GCC CCT GAC TTA GGA CAG AGA ACC CCA GGG GCC AAG CCA GGG TTG	447
Gly Ala Pro Asp Leu Gly Gln Arg Thr Pro Gly Ala Lys Pro Gly Leu	
30 35 40	
ACC AAA GCG GAG GCC AAG GAG AGG CCA CCC CTG GCC AGG AAT GTC TTT	495
Thr Lys Ala Glu Ala Lys Glu Arg Pro Pro Leu Ala Arg Asn Val Phe	
45 50 55	
AGG CCA GGG GGT CAT ATC TAT GGT GTG GGG GCC ACC AAT GCC AGG GCC	543
Arg Pro Gly Gly His Ile Tyr Gly Val Gly Ala Thr Asn Ala Arg Ala	
60 65 70	
AAG GGA AGC TCT GGG CAG ACA CAG GCC AAG AAG GAT GAA CCC AGA AAG	591
Lys Gly Ser Ser Gly Gln Thr Gln Ala Lys Lys Asp Glu Pro Arg Lys	
75 80 85 90	
ATG CCC CCC AGA TCC GGT GGC TCT GAA ACC AAG CCA GGA CCC TCT TCC	639

Met	Pro	Pro	Arg	Ser	Gly	Gly	Ser	Glu	Thr	Lys	Pro	Gly	Pro	Ser	Ser	
				95					100					105		
CAG	ACT	AGA	CAG	GCT	GCA	GCC	CGG	ACT	GTA	ACC	CCA	AAA	GGA	CAG	CTT	687
Gln	Thr	Arg	Gln	Ala	Ala	Ala	Arg	Thr	Val	Thr	Pro	Lys	Gly	Gln	Leu	
			110					115					120			
CCT	GGG	GGC	AAA	GCA	TCT	TCA	AAA	GCA	GGA	TCT	GCC	CCC	AGC	TCC	TTC	735
Pro	Gly	Gly	Lys	Ala	Ser	Ser	Lys	Ala	Gly	Ser	Ala	Pro	Ser	Ser	Phe	
			125				130					135				
CTG	CTG	AAG	AAG	ACC	AGG	GAG	CCT	GGG	ACC	CCT	CGA	GAG	CCC	AAG	GAG	783
Leu	Leu	Lys	Lys	Thr	Arg	Glu	Pro	Gly	Thr	Pro	Arg	Glu	Pro	Lys	Glu	
	140					145					150					
CCG	TTC	CGC	CCG	CCC	CCC	ATC	ACA	CCC	CAC	GAA	TAC	ATG	CTC	TCC	CTG	831
Pro	Phe	Arg	Pro	Pro	Pro	Ile	Thr	Pro	His	Glu	Tyr	Met	Leu	Ser	Leu	
155					160					165					170	
TAC	AGG	ACG	CTG	TCC	GAT	GCT	GAC	AGA	AAG	GGA	GGT	AAC	AGC	AGC	GTG	879
Tyr	Arg	Thr	Leu	Ser	Asp	Ala	Asp	Arg	Lys	Gly	Gly	Asn	Ser	Ser	Val	
				175					180					185		
AAG	TTG	GAG	GCT	GGC	CTG	GCC	AAC	ACC	ATC	ACC	AGC	TTT	ATT	GAC	AAA	927
Lys	Leu	Glu	Ala	Gly	Leu	Ala	Asn	Thr	Ile	Thr	Ser	Phe	Ile	Asp	Lys	
			190					195					200			
GGG	CAA	GAT	GAC	CGA	GGC	CCT	GCG	GTC	AGG	AAG	CAG	AGG	TAC	GTG	TTT	975
Gly	Gln	Asp	Asp	Arg	Gly	Pro	Ala	Val	Arg	Lys	Gln	Arg	Tyr	Val	Phe	
		205					210					215				
GAC	ATC	AGT	GCC	TTG	GAG	AAG	GAT	GGG	CTG	TTG	GGG	GCT	GAA	CTG	CGG	1023
Asp	Ile	Ser	Ala	Leu	Glu	Lys	Asp	Gly	Leu	Leu	Gly	Ala	Glu	Leu	Arg	
	220					225					230					
ATC	TTA	CGG	AAG	AAG	CCC	TTG	GAC	GTG	GCC	AAG	CCA	GCG	GTC	CCC	AGT	1071
Ile	Leu	Arg	Lys	Lys	Pro	Leu	Asp	Val	Ala	Lys	Pro	Ala	Val	Pro	Ser	
235					240					245					250	
AGC	GGG	CGG	GTT	GCC	CAA	CTG	AAG	CTG	TCC	AGC	TGC	CCC	AGC	GGC	CGG	1119
Ser	Gly	Arg	Val	Ala	Gln	Leu	Lys	Leu	Ser	Ser	Cys	Pro	Ser	Gly	Arg	
				255					260					265		
CAG	CCG	GCA	GCC	TTG	CTG	GAT	GTG	CGC	TCC	GTG	CCA	GGC	CTG	GAT	GGA	1167
Gln	Pro	Ala	Ala	Leu	Leu	Asp	Val	Arg	Ser	Val	Pro	Gly	Leu	Asp	Gly	
			270					275					280			
TCT	GGC	TGG	GAG	GTG	TTC	GAC	ATC	TGG	AAG	CTC	TTC	CGA	AAT	TTT	AAG	1215
Ser	Gly	Trp	Glu	Val	Phe	Asp	Ile	Trp	Lys	Leu	Phe	Arg	Asn	Phe	Lys	
		285					290					295				
AAC	TCA	GCG	CAG	CTG	TGC	CTG	GAG	CTG	GAG	GCC	TGG	GAA	CGG	GGC	CGG	1263
Asn	Ser	Ala	Gln	Leu	Cys	Leu	Glu	Leu	Glu	Ala	Trp	Glu	Arg	Gly	Arg	
	300					305					310					

GCC GTG GAC CTC CGT GGC CTG GGC TTT GAA CGC ACT GCC CGA CAG GTC	1311
Ala Val Asp Leu Arg Gly Leu Gly Phe Glu Arg Thr Ala Arg Gln Val	
315 320 325 330	
CAC GAG AAA GCC TTG TTC CTA GTG TTT GGT CGT ACC AAG AAA CGG GAC	1359
His Glu Lys Ala Leu Phe Leu Val Phe Gly Arg Thr Lys Lys Arg Asp	
335 340 345	
CTG TTC TTT AAT GAG ATT AAG GCC CGC TCT GGC CAG GAT GAC AAG ACT	1407
Leu Phe Phe Asn Glu Ile Lys Ala Arg Ser Gly Gln Asp Asp Lys Thr	
350 355 360	
GTG TAT GAA TAT TTG TTC AGC CAG CGG CGG AAA CGC CGG GCC CCA TTG	1455
Val Tyr Glu Tyr Leu Phe Ser Gln Arg Arg Lys Arg Arg Ala Pro Leu	
365 370 375	
GCC AAT CGC CAG GGC AAG CGA CCC AGC AAG AAC CTC AAG GCT CGC TGC	1503
Ala Asn Arg Gln Gly Lys Arg Pro Ser Lys Asn Leu Lys Ala Arg Cys	
380 385 390	
AGT CGC AAG GCC TTG CAT GTC AAC TTC AAG GAC ATG GGC TGG GAC GAC	1551
Ser Arg Lys Ala Leu His Val Asn Phe Lys Asp Met Gly Trp Asp Asp	
395 400 405 410	
TGG ATC ATC GCA CCT CTT GAG TAT GAG GCC TTC CAC TGC GAA GGA CTG	1599
Trp Ile Ile Ala Pro Leu Glu Tyr Glu Ala Phe His Cys Glu Gly Leu	
415 420 425	
TGT GAG TTC CCC TTG CGC TCC CAC TTG GAG CCC ACA AAC CAC GCA GTC	1647
Cys Glu Phe Pro Leu Arg Ser His Leu Glu Pro Thr Asn His Ala Val	
430 435 440	
ATT CAG ACC CTA ATG AAC TCT ATG GAC CCT GAA TCC ACA CCA CCC ACT	1695
Ile Gln Thr Leu Met Asn Ser Met Asp Pro Glu Ser Thr Pro Pro Thr	
445 450 455	
TGT TGT GTG CCT ACA CGG CTG AGT CCT ATT AGC ATC CTC TTC ATC GAC	1743
Cys Cys Val Pro Thr Arg Leu Ser Pro Ile Ser Ile Leu Phe Ile Asp	
460 465 470	
TCT GCC AAC AAC GTG GTG TAT AAA CAG TAC GAG GAC ATG GTC GTG GAA	1791
Ser Ala Asn Asn Val Val Tyr Lys Gln Tyr Glu Asp Met Val Val Glu	
475 480 485 490	
TCT TGT GGC TGC AGG TAGCAGCACC GGCCACCTG TCTTCCAGGG TGGCACATCC A	1847
Ser Cys Gly Cys Arg	
495	
GAGACTACCC CCTCTACAGG TTCCTGGAGT AACAGAGAGC CTGTGAAGCT GCTGCCCCGAA	1907
GTTTCCTGGC AGCCTGCAGG AAAGAGTTCT CAGCAGGCTT ACTCTCTGGA TGTGATCTGG	1967
ACTAAAGAGA TCACCTTCTG AAGATTCTTG CCCAAGGAAC AGACTCTGAG TGGGCTGGG	2027
GCTCAGGAAA GGTGTTCTTA ATGAGATTCA GTTCACCATC TCTCCTGCCG GGGCCGAGGA	2087
CCTTCATTTT TCTCCAGACT CTCCAGAGAA GTTGTAGCTA TATCCTAAGC TCTTTAAGGG	2147
AGAGCTGTCT CCTCCTTGAA TCACCTTTGT GCCTGGTGAC TTTCTGCCAC GAGATGTTCA	2207
TTACAGGGGC TGGGCAAAGA AGGGGAAAGG GCTTGGGCAG GGGTGAAGAG AAGAGTATGA	2267

GCCTAATTAG ACTGTTAGAT TAAAATGTAC ATCGATGACA TAAAAGCTGA ATCTTCATGG 2327
CT 2329

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 495 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met	Arg	Leu	Pro	Lys	Leu	Leu	Thr	Leu	Leu	Leu	Trp	His	Leu	Ala	Trp
1				5				10						15	
Leu	Asp	Leu	Glu	Leu	Ile	Cys	Thr	Val	Leu	Gly	Ala	Pro	Asp	Leu	Gly
		20						25					30		
Gln	Arg	Thr	Pro	Gly	Ala	Lys	Pro	Gly	Leu	Thr	Lys	Ala	Glu	Ala	Lys
		35					40					45			
Glu	Arg	Pro	Pro	Leu	Ala	Arg	Asn	Val	Phe	Arg	Pro	Gly	Gly	His	Ile
	50					55					60				
Tyr	Gly	Val	Gly	Ala	Thr	Asn	Ala	Arg	Ala	Lys	Gly	Ser	Ser	Gly	Gln
65					70					75					80
Thr	Gln	Ala	Lys	Lys	Asp	Glu	Pro	Arg	Lys	Met	Pro	Pro	Arg	Ser	Gly
			85					90						95	
Gly	Ser	Glu	Thr	Lys	Pro	Gly	Pro	Ser	Gln	Thr	Arg	Gln	Ala	Ala	
		100					105					110			
Ala	Arg	Thr	Val	Thr	Pro	Lys	Gly	Gln	Leu	Pro	Gly	Gly	Lys	Ala	Ser
	115					120					125				
Ser	Lys	Ala	Gly	Ser	Ala	Pro	Ser	Ser	Phe	Leu	Leu	Lys	Lys	Thr	Arg
	130					135				140					
Glu	Pro	Gly	Thr	Pro	Arg	Glu	Pro	Lys	Glu	Pro	Phe	Arg	Pro	Pro	Pro
145				150					155						160
Ile	Thr	Pro	His	Glu	Tyr	Met	Leu	Ser	Leu	Tyr	Arg	Thr	Leu	Ser	Asp
			165					170						175	
Ala	Asp	Arg	Lys	Gly	Gly	Asn	Ser	Ser	Val	Lys	Leu	Glu	Ala	Gly	Leu
		180				185							190		
Ala	Asn	Thr	Ile	Thr	Ser	Phe	Ile	Asp	Lys	Gly	Gln	Asp	Asp	Arg	Gly
	195					200					205				
Pro	Ala	Val	Arg	Lys	Gln	Arg	Tyr	Val	Phe	Asp	Ile	Ser	Ala	Leu	Glu
	210				215					220					
Lys	Asp	Gly	Leu	Leu	Gly	Ala	Glu	Leu	Arg	Ile	Leu	Arg	Lys	Lys	Pro
225				230					235						240
Leu	Asp	Val	Ala	Lys	Pro	Ala	Val	Pro	Ser	Gly	Arg	Val	Ala	Gln	
			245					250					255		
Leu	Lys	Leu	Ser	Cys	Pro	Ser	Gly	Arg	Gln	Pro	Ala	Ala	Leu	Leu	
		260				265					270				
Asp	Val	Arg	Ser	Val	Pro	Gly	Leu	Asp	Gly	Ser	Gly	Trp	Glu	Val	Phe
	275					280					285				
Asp	Ile	Trp	Lys	Leu	Phe	Arg	Asn	Phe	Lys	Asn	Ser	Ala	Gln	Leu	Cys

290		295		300											
Leu	Glu	Leu	Glu	Ala	Trp	Glu	Arg	Gly	Arg	Ala	Val	Asp	Leu	Arg	Gly
305				310						315					320
Leu	Gly	Phe	Glu	Arg	Thr	Ala	Arg	Gln	Val	His	Glu	Lys	Ala	Leu	Phe
				325						330					335
Leu	Val	Phe	Gly	Arg	Thr	Lys	Lys	Arg	Asp	Leu	Phe	Phe	Asn	Glu	Ile
			340						345					350	
Lys	Ala	Arg	Ser	Gly	Gln	Asp	Asp	Lys	Thr	Val	Tyr	Glu	Tyr	Leu	Phe
		355					360					365			
Ser	Gln	Arg	Arg	Lys	Arg	Arg	Ala	Pro	Leu	Ala	Asn	Arg	Gln	Gly	Lys
		370				375					380				
Arg	Pro	Ser	Lys	Asn	Leu	Lys	Ala	Arg	Cys	Ser	Arg	Lys	Ala	Leu	His
385				390						395					400
Val	Asn	Phe	Lys	Asp	Met	Gly	Trp	Asp	Asp	Trp	Ile	Ile	Ala	Pro	Leu
			405						410						415
Glu	Tyr	Glu	Ala	Phe	His	Cys	Glu	Gly	Leu	Cys	Glu	Phe	Pro	Leu	Arg
			420					425					430		
Ser	His	Leu	Glu	Pro	Thr	Asn	His	Ala	Val	Ile	Gln	Thr	Leu	Met	Asn
		435					440					445			
Ser	Met	Asp	Pro	Glu	Ser	Thr	Pro	Pro	Thr	Cys	Cys	Val	Pro	Thr	Arg
	450					455				460					
Leu	Ser	Pro	Ile	Ser	Ile	Leu	Phe	Ile	Asp	Ser	Ala	Asn	Asn	Val	Val
465				470					475						480
Tyr	Lys	Gln	Tyr	Glu	Asp	Met	Val	Val	Glu	Ser	Cys	Gly	Cys	Arg	
				485					490					495	

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

- (B) CLONE: GDF-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Arg	Leu	Arg	Arg	His	Thr	Glu	Pro	Arg	Val	Glu	Val	Gly	Pro	Val	Gly
1				5					10					15	
Thr	Cys	Arg	Thr	Arg	Arg	Leu	His	Val	Ser	Phe	Arg	Glu	Val	Gly	Trp
		20						25				30			
His	Arg	Trp	Val	Ile	Ala	Pro	Arg	Gly	Phe	Leu	Ala	Asn	Phe	Cys	Gln
		35				40					45				
Gly	Thr	Cys	Ala	Leu	Pro	Glu	Thr	Leu	Arg	Gly	Pro	Gly	Gly	Pro	Pro
	50				55				60						
Ala	Leu	Asn	His	Ala	Val	Leu	Arg	Ala	Leu	Met	His	Ala	Ala	Ala	Pro
65				70					75						80
Thr	Pro	Gly	Ala	Gly	Ser	Pro	Cys	Cys	Val	Pro	Glu	Arg	Leu	Ser	Pro
			85					90					95		
Ile	Ser	Val	Leu	Phe	Phe	Asp	Asn	Glu	Asp	Asn	Val	Val	Leu	Arg	His

100 105 110
 Tyr Glu Asp Met Val Val Asp Glu Cys Gly Cys Arg
 115 120

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

- (B) CLONE: GDF-3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Arg	Lys	Arg	Arg	Ala	Ala	Ile	Ser	Val	Pro	Lys	Gly	Phe	Cys	Arg	Asn
1				5					10					15	
Phe	Cys	His	Arg	His	Gln	Leu	Phe	Ile	Asn	Phe	Gln	Asp	Leu	Gly	Trp
			20					25					30		
His	Lys	Trp	Val	Ile	Ala	Pro	Lys	Gly	Phe	Met	Ala	Asn	Tyr	Cys	His
		35					40					45			
Gly	Glu	Cys	Pro	Phe	Ser	Met	Thr	Thr	Tyr	Leu	Asn	Ser	Ser	Asn	Tyr
	50					55					60				
Ala	Phe	Met	Gln	Ala	Leu	Met	His	Met	Ala	Asp	Pro	Lys	Val	Pro	Lys
65					70					75					80
Ala	Val	Cys	Val	Pro	Thr	Lys	Leu	Ser	Pro	Ile	Ser	Met	Leu	Tyr	Gln
				85					90					95	
Asp	Ser	Asp	Lys	Asn	Val	Ile	Leu	Arg	His	Tyr	Glu	Asp	Met	Val	Val
			100					105					110		
Asp	Glu	Cys	Gly	Cys	Gly										
			115												

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

- (B) CLONE: GDF-5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Pro	Leu	Ala	Asn	Arg	Gln	Gly	Lys	Arg	Pro	Ser	Lys	Asn	Leu	Lys	Ala
1				5					10					15	
Arg	Cys	Ser	Arg	Lys	Ala	Leu	His	Val	Asn	Phe	Lys	Asp	Met	Gly	Trp

	20		25		30										
Asp	Asp	Trp	Ile	Ile	Ala	Pro	Leu	Glu	Tyr	Glu	Ala	Phe	His	Cys	Glu
	35						40						45		
Gly	Leu	Cys	Glu	Phe	Pro	Leu	Arg	Ser	His	Leu	Glu	Pro	Thr	Asn	His
	50						55						60		
Ala	Val	Ile	Gln	Thr	Leu	Met	Asn	Ser	Met	Asp	Pro	Glu	Ser	Thr	Pro
	65						70						75		80
Pro	Thr	Cys	Cys	Val	Pro	Thr	Arg	Leu	Ser	Pro	Ile	Ser	Ile	Leu	Phe
							85						90		95
Ile	Asp	Ser	Ala	Asn	Asn	Val	Val	Tyr	Lys	Gln	Tyr	Glu	Asp	Met	Val
									100				105		110
Val	Glu	Ser	Cys	Gly	Cys	Arg									
															115

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ~~protein~~

(vii) IMMEDIATE SOURCE:

- (B) CLONE: GDF-9

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Ser	Phe	Asn	Leu	Ser	Glu	Tyr	Phe	Lys	Gln	Phe	Leu	Phe	Pro	Gln	Asn
1					5				10					15	
Glu	Cys	Glu	Leu	His	Asp	Phe	Arg	Leu	Ser	Phe	Ser	Gln	Leu	Lys	Trp
			20						25				30		
Asp	Asn	Trp	Ile	Val	Ala	Pro	His	Arg	Tyr	Asn	Pro	Arg	Tyr	Cys	Lys
			35						40				45		
Gly	Asp	Cys	Pro	Arg	Ala	Val	Arg	His	Arg	Tyr	Gly	Ser	Pro	Val	His
	50						55						60		
Thr	Met	Val	Gln	Asn	Ile	Ile	Tyr	Glu	Lys	Leu	Asp	Pro	Ser	Val	Pro
	65						70				75				80
Arg	Pro	Ser	Cys	Val	Pro	Gly	Lys	Tyr	Ser	Pro	Leu	Ser	Val	Leu	Thr
							85				90				95
Ile	Glu	Pro	Asp	Gly	Ser	Ile	Ala	Tyr	Lys	Glu	Tyr	Glu	Asp	Met	Ile
			100						105				110		
Ala	Thr	Arg	Cys	Thr	Cys	Arg									
															115

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

(B) CLONE: BMP-2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

```

Arg Glu Lys Arg Gln Ala Lys His Lys Gln Arg Lys Arg Leu Lys Ser
 1           5           10           15
Ser Cys Lys Arg His Pro Leu Tyr Val Asp Phe Ser Asp Val Gly Trp
          20           25           30
Asn Asp Trp Ile Val Ala Pro Pro Gly Tyr His Ala Phe Tyr Cys His
          35           40           45
Gly Glu Cys Pro Phe Pro Leu Ala Asp His Leu Asn Ser Thr Asn His
          50           55           60
Ala Ile Val Gln Thr Leu Val Asn Ser Val Asn Ser Lys Ile Pro Lys
          65           70           75           80
Ala Cys Cys Val Pro Thr Glu Leu Ser Ala Ile Ser Met Leu Tyr Leu
          85           90           95
Asp Glu Asn Glu Lys Val Val Leu Lys Asn Tyr Gln Asp Met Val Val
          100          105          110
Glu Gly Cys Gly Cys Arg
          115

```

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 118 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

(B) CLONE: BMP-4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

```

Lys Arg Ser Pro Lys His His Ser Gln Arg Ala Arg Lys Lys Asn Lys
 1           5           10           15
Asn Cys Arg Arg His Ser Leu Tyr Val Asp Phe Ser Asp Val Gly Trp
          20           25           30
Asn Asp Trp Ile Val Ala Pro Pro Gly Tyr Gln Ala Phe Tyr Cys His
          35           40           45
Gly Asp Cys Pro Phe Pro Leu Ala Asp His Leu Asn Ser Thr Asn His
          50           55           60
Ala Ile Val Gln Thr Leu Val Asn Ser Val Asn Ser Ser Ile Pro Lys
          65           70           75           80
Ala Cys Cys Val Pro Thr Glu Leu Ser Ala Ile Ser Met Leu Tyr Leu
          85           90           95
Asp Glu Tyr Asp Lys Val Val Leu Lys Asn Tyr Gln Glu Met Val Val
          100          105          110
Glu Gly Cys Gly Cys Arg

```

115

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

- (B) CLONE: Vgr-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Ser	Arg	Gly	Ser	Gly	Ser	Ser	Asp	Tyr	Asn	Gly	Ser	Glu	Leu	Lys	Thr
1				5					10					15	
Ala	Cys	Lys	Lys	His	Glu	Leu	Tyr	Val	Ser	Phe	Gln	Asp	Leu	Gly	Trp
		20					25						30		
Gln	Asp	Trp	Ile	Ile	Ala	Pro	Lys	Gly	Tyr	Ala	Ala	Asn	Tyr	Cys	Asp
	35						40					45			
Gly	Glu	Cys	Ser	Phe	Pro	Leu	Asn	Ala	His	Met	Asn	Ala	Thr	Asn	His
	50					55					60				
Ala	Ile	Val	Gln	Thr	Leu	Val	His	Leu	Met	Asn	Pro	Glu	Tyr	Val	Pro
65					70				75					80	
Lys	Pro	Cys	Cys	Ala	Pro	Thr	Lys	Leu	Asn	Ala	Ile	Ser	Val	Leu	Tyr
			85					90						95	
Phe	Asp	Asp	Asn	Ser	Asn	Val	Ile	Leu	Lys	Lys	Tyr	Arg	Asn	Met	Val
			100					105					110		
Val	Arg	Ala	Cys	Gly	Cys	His									
			115												

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

- (B) CLONE: OP-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Leu	Arg	Met	Ala	Asn	Val	Ala	Glu	Asn	Ser	Ser	Ser	Asp	Gln	Arg	Gln
1				5					10					15	
Ala	Cys	Lys	Lys	His	Glu	Leu	Tyr	Val	Ser	Phe	Arg	Asp	Leu	Gly	Trp
		20					25						30		
Gln	Asp	Trp	Ile	Ile	Ala	Pro	Glu	Gly	Tyr	Ala	Ala	Tyr	Tyr	Cys	Glu

```

      35          40          45
Gly Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met Asn Ala Thr Asn His
   50          55          60
Ala Ile Val Gln Thr Leu Val His Phe Ile Asn Pro Glu Thr Val Pro
   65          70          75          80
Lys Pro Cys Cys Ala Pro Thr Gln Leu Asn Ala Ile Ser Val Leu Tyr
      85          90          95
Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys Tyr Arg Asn Met Val
      100          105          110
Val Arg Ala Cys Gly Cys His
      115

```

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

- (B) CLONE: BMP-5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

```

Ser Arg Met Ser Ser Val Gly Asp Tyr Asn Thr Ser Glu Gln Lys Gln
 1          5          10          15
Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe Arg Asp Leu Gly Trp
      20          25          30
Gln Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala Ala Phe Tyr Cys Asp
      35          40          45
Gly Glu Cys Ser Phe Pro Leu Asn Ala His Met Asn Ala Thr Asn His
   50          55          60
Ala Ile Val Gln Thr Leu Val His Leu Met Phe Pro Asp His Val Pro
   65          70          75          80
Lys Pro Cys Cys Ala Pro Thr Lys Leu Asn Ala Ile Ser Val Leu Tyr
      85          90          95
Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys Tyr Arg Asn Met Val
      100          105          110
Val Arg Ser Cys Gly Cys His
      115

```

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

(B) CLONE: BMP-3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

```

Glu Gln Thr Leu Lys Lys Ala Arg Arg Lys Gln Trp Ile Glu Pro Arg
 1           5           10           15
Asn Cys Ala Arg Arg Tyr Leu Lys Val Asp Phe Ala Asp Ile Gly Trp
      20           25           30
Ser Glu Trp Ile Ile Ser Pro Lys Ser Phe Asp Ala Tyr Tyr Cys Ser
      35           40           45
Gly Ala Cys Gln Phe Pro Met Pro Lys Ser Leu Lys Pro Ser Asn His
      50           55           60
Ala Thr Ile Gln Ser Ile Val Arg Ala Val Gly Val Val Pro Gly Ile
      65           70           75           80
Pro Glu Pro Cys Cys Val Pro Glu Lys Met Ser Ser Leu Ser Ile Leu
      85           90           95
Phe Phe Asp Glu Asn Lys Asn Val Val Leu Lys Val Tyr Pro Asn Met
      100          105          110
Thr Val Glu Ser Cys Ala Cys Arg
      115          120

```

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 116 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

(B) CLONE: MIS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

```

Gly Pro Gly Arg Ala Gln Arg Ser Ala Gly Ala Thr Ala Ala Asp Gly
 1           5           10           15
Pro Cys Ala Leu Arg Glu Leu Ser Val Asp Leu Arg Ala Glu Arg Ser
      20           25           30
Val Leu Ile Pro Glu Thr Tyr Gln Ala Asn Asn Cys Gln Gly Val Cys
      35           40           45
Gly Trp Pro Gln Ser Asp Arg Asn Pro Arg Tyr Gly Asn His Val Val
      50           55           60
Leu Leu Leu Lys Met Gln Ala Arg Gly Ala Ala Leu Ala Arg Pro Pro
      65           70           75           80
Cys Cys Val Pro Thr Ala Tyr Ala Gly Lys Leu Leu Ile Ser Leu Ser
      85           90           95
Glu Glu Arg Ile Ser Ala His His Val Pro Asn Met Val Ala Thr Glu
      100          105          110
Cys Gly Cys Arg
      115

```

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

- (B) CLONE: Inhibit-alpha

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Ala Leu Arg Leu Leu Gln Arg Pro Pro Glu Glu Pro Ala Ala His Ala
 1 5 10 15
 Asn Cys His Arg Val Ala Leu Asn Ile Ser Phe Gln Glu Leu Gly Trp
 20 25 30
 Glu Arg Trp Ile Val Tyr Pro Pro Ser Phe Ile Phe His Tyr Cys His
 35 40 45
 Gly Gly Cys Gly Leu His Ile Pro Pro Asn Leu Ser Leu Pro Val Pro
 50 55 60
~~Gly Ala Pro Pro Thr Pro Ala Gln Pro Tyr Ser Leu Leu Pro Gly Ala~~
~~65 70 75 80~~
 Gln Pro Cys Cys Ala Ala Leu Pro Gly Thr Met Arg Pro Leu His Val
 85 90 95
 Arg Thr Thr Ser Asp Gly Gly Tyr Ser Phe Lys Tyr Glu Thr Val Pro
 100 105 110
 Asn Leu Leu Thr Gln His Cys Ala Cys Ile
 115 120

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

- (B) CLONE: Inhibit-beta-alpha

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

His Arg Arg Arg Arg Arg Gly Leu Glu Cys Asp Gly Lys Val Asn Ile
 1 5 10 15
 Cys Cys Lys Lys Gln Phe Phe Val Ser Phe Lys Asp Ile Gly Trp Asn
 20 25 30
 Asp Trp Ile Ile Ala Pro Ser Gly Tyr His Ala Asn Tyr Cys Glu Gly
 35 40 45
 Glu Cys Pro Ser His Ile Ala Gly Thr Ser Gly Ser Ser Leu Ser Phe
 50 55 60

His Ser Thr Val Ile Asn His Tyr Arg Met Arg Gly His Ser Pro Phe
65 70 75 80
Ala Asn Leu Lys Ser Cys Cys Val Pro Thr Lys Leu Arg Pro Met Ser
85 90 95
Met Leu Tyr Tyr Asp Asp Gly Gln Asn Ile Ile Lys Lys Asp Ile Gln
100 105 110
Asn Met Ile Val Glu Glu Cys Gly Cys Ser
115 120

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

- (B) CLONE: Inhibit-beta-beta

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

His Arg Ile Arg Lys Arg Gly Leu Glu Cys Asp Gly Arg Thr Asn Leu
1 5 10 15
Cys Cys Arg Gln Gln Phe Phe Ile Asp Phe Arg Leu Ile Gly Trp Asn
20 25 30
Asp Trp Ile Ile Ala Pro Thr Gly Tyr Tyr Gly Asn Tyr Cys Glu Gly
35 40 45
Ser Cys Pro Ala Tyr Leu Ala Gly Val Pro Gly Ser Ala Ser Ser Phe
50 55 60
His Thr Ala Val Val Asn Gln Tyr Arg Met Arg Gly Leu Asn Pro Gly
65 70 75 80
Thr Val Asn Ser Cys Cys Ile Pro Thr Lys Leu Ser Thr Met Ser Met
85 90 95
Leu Tyr Phe Asp Asp Glu Tyr Asn Ile Val Lys Arg Asp Val Pro Asn
100 105 110
Met Ile Val Glu Glu Cys Gly Cys Ala
115 120

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

- (B) CLONE: TGF-beta-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

```

His Arg Arg Ala Leu Asp Thr Asn Tyr Cys Phe Ser Ser Thr Glu Lys
 1           5           10           15
Asn Cys Cys Val Arg Gln Leu Tyr Ile Asp Phe Arg Lys Asp Leu Gly
          20           25           30
Trp Lys Trp Ile His Glu Pro Lys Gly Tyr His Ala Asn Phe Cys Leu
          35           40           45
Gly Pro Cys Pro Tyr Ile Trp Ser Leu Asp Thr Gln Tyr Ser Lys Val
          50           55           60
Leu Ala Leu Tyr Asn Gln His Asn Pro Gly Ala Ser Ala Ala Pro Cys
          65           70           75           80
Cys Val Pro Gln Ala Leu Glu Pro Leu Pro Ile Val Tyr Tyr Val Gly
          85           90           95
Arg Lys Pro Lys Val Glu Gln Leu Ser Asn Met Ile Val Arg Ser Cys
          100          105          110
Lys Cys Ser
          115

```

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

- (B) CLONE: TGF-beta-2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

```

Lys Lys Arg Ala Leu Asp Ala Ala Tyr Cys Phe Arg Asn Val Gln Asp
 1           5           10           15
Asn Cys Cys Leu Arg Pro Leu Tyr Ile Asp Phe Lys Arg Asp Leu Gly
          20           25           30
Trp Lys Trp Ile His Glu Pro Lys Gly Tyr Asn Ala Asn Phe Cys Ala
          35           40           45
Gly Ala Cys Pro Tyr Leu Trp Ser Ser Asp Thr Gln His Ser Arg Val
          50           55           60
Leu Ser Leu Tyr Asn Thr Ile Asn Pro Glu Ala Ser Ala Ser Pro Cys
          65           70           75           80
Cys Val Ser Gln Asp Leu Glu Pro Leu Thr Ile Leu Tyr Tyr Ile Gly
          85           90           95
Lys Thr Pro Lys Ile Glu Gln Leu Ser Asn Met Ile Val Lys Ser Cys
          100          105          110
Lys Cys Ser
          115

```

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

- (B) CLONE: TGF-beta-3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Lys Lys Arg Ala Leu Asp Thr Asn Tyr Cys Phe Arg Asn Leu Glu Glu
 1 5 10 15
 Asn Cys Cys Val Arg Pro Leu Tyr Ile Asp Phe Arg Gln Asp Leu Gly
 20 25 30
 Trp Lys Trp Val His Glu Pro Lys Gly Tyr Tyr Ala Asn Phe Cys Ser
 35 40 45
 Gly Pro Cys Pro Tyr Leu Arg Ser Ala Asp Thr Thr His Ser Thr Val
 50 55 60
 Leu Gly Leu Tyr Asn Thr Leu Asn Pro Glu Ala Ser Ala Ser Pro Cys
 65 70 75 80
~~Cys Val Pro Gln Asp Leu Glu Pro Leu Thr Ile Leu Tyr Tyr Val Gly~~
~~85 90 95~~
 Arg Thr Pro Lys Val Glu Gln Leu Ser Asn Met Val Val Lys Ser Cys
 100 105 110
 Lys Cys Ser
 115